SEQUENCE LISTING

<110> IKADAI, Hiromi et al.

<120> GENE ENCODING PROTEIN FROM MEROZOITE OF BABESIA CABALLI, RECOMBINANT PROTEIN OBTAINED WITH SAID GENE AND USE THEREOF

<130> 0020-4843P

<140> 09/807,459
<141> 2001-04-13

<160> 2

<170> PatentIn version 3.0

B1

<210> 1
<211> 1828
<212> DNA
<213> Babesia caballi

<220>
<221> CDS
<222> (39)..(1412)

<400> 1

```
gtgccctggc cgttcgccac aacagccgtg tttccatc atg gct ccc agc gac tct      56
                                        Met Ala Pro Ser Asp Ser
                                        1               5

gtg ggc gac gtg act aag acc tta ttg gct gcc agc gaa agt gtg gac      104
Val Gly Asp Val Thr Lys Thr Leu Leu Ala Ala Ser Glu Ser Val Asp
            10                  15                  20

tca gct gcc aat gcc tat atg atc aac agt gac atg agc gat tac ttg      152
Ser Ala Ala Asn Ala Tyr Met Ile Asn Ser Asp Met Ser Asp Tyr Leu
        25                  30                  35

tcg gct gtg tct gac aac ttc gcc gag cgc att tgc agt cag gtc cct      200
Ser Ala Val Ser Asp Asn Phe Ala Glu Arg Ile Cys Ser Gln Val Pro
    40                  45                  50

aag ggg agt aac tgc agt gct tcc gtt agc gca tac atg agt cgc tgc      248
Lys Gly Ser Asn Cys Ser Ala Ser Val Ser Ala Tyr Met Ser Arg Cys
55                  60                  65                  70

gct aaa cag gac tgc ctg act ctc caa agt ctt aag tac cct ctt gag      296
Ala Lys Gln Asp Cys Leu Thr Leu Gln Ser Leu Lys Tyr Pro Leu Glu
                75                  80                  85

gct aag tac caa ccg ctg acc ctt cct gac ccc tac cag ttg gag gcc      344
Ala Lys Tyr Gln Pro Leu Thr Leu Pro Asp Pro Tyr Gln Leu Glu Ala
            90                  95                  100
```

```
gca ttt ata ctc ttc aag gag agt gac gct aat ccg gcc aat agc act      392
Ala Phe Ile Leu Phe Lys Glu Ser Asp Ala Asn Pro Ala Asn Ser Thr
        105                 110                 115

gag aag cgc ttc tgg atg cgt ttc aga agg ggc aag aac cac agt tac      440
Glu Lys Arg Phe Trp Met Arg Phe Arg Arg Gly Lys Asn His Ser Tyr
    120                 125                 130

ttc cac gac tta gtc ttc aat ctg ctg gag aag aac gtg act cgc gac      488
Phe His Asp Leu Val Phe Asn Leu Leu Glu Lys Asn Val Thr Arg Asp
135                 140                 145                 150

gcg gat gct act gac att gag aac ttt gcg tcc agg tac ctg tac atg      536
Ala Asp Ala Thr Asp Ile Glu Asn Phe Ala Ser Arg Tyr Leu Tyr Met
                155                 160                 165

gcc acg ctt tac tac aag acg tac acg aat gtt gat gag ttc ggt gct      584
Ala Thr Leu Tyr Tyr Lys Thr Tyr Thr Asn Val Asp Glu Phe Gly Ala
            170                 175                 180

agc ttc ttt aac aag ttg tct ttc act act ggg ttg ttc ggc tgg ggc      632
Ser Phe Phe Asn Lys Leu Ser Phe Thr Thr Gly Leu Phe Gly Trp Gly
        185                 190                 195

atc aag agg gca ctt aag cag att att cgc tct aac ctg ccc ctt gac      680
Ile Lys Arg Ala Leu Lys Gln Ile Ile Arg Ser Asn Leu Pro Leu Asp
    200                 205                 210

atc ggg aca gaa cac agc gtc agt cgc ctg cag cac att acg agc agt      728
Ile Gly Thr Glu His Ser Val Ser Arg Leu Gln His Ile Thr Ser Ser
215                 220                 225                 230

tac aag gat tac atg gat acg cag att cct gca ctg ccc aag ttt gcg      776
Tyr Lys Asp Tyr Met Asp Thr Gln Ile Pro Ala Leu Pro Lys Phe Ala
                235                 240                 245

aag cgt ttc tcc ctt atg gta gtg cag agg ctg ctg gcc acc gtg gct      824
Lys Arg Phe Ser Leu Met Val Val Gln Arg Leu Leu Ala Thr Val Ala
            250                 255                 260

ggt tac gtc gac acc ccg tgg tat aag aag tgg tac atg aag ctg aag      872
Gly Tyr Val Asp Thr Pro Trp Tyr Lys Lys Trp Tyr Met Lys Leu Lys
        265                 270                 275

aac ttt atg gtg aac agg gtg ttc att cct aca aag aag ttc ttc aat      920
Asn Phe Met Val Asn Arg Val Phe Ile Pro Thr Lys Lys Phe Phe Asn
    280                 285                 290

aag gaa att cgt gag cct agt aag gca tta aaa gaa aag gtg tca acc      968
Lys Glu Ile Arg Glu Pro Ser Lys Ala Leu Lys Glu Lys Val Ser Thr
295                 300                 305                 310

gac acc aag gat tta ttc gag aac aaa att ggg cag ggt act gtg gac     1016
Asp Thr Lys Asp Leu Phe Glu Asn Lys Ile Gly Gln Gly Thr Val Asp
                315                 320                 325
```

```
ttc ttc aat aag gaa att cgt gac cct agt aag gca tta aaa gaa aaa     1064
Phe Phe Asn Lys Glu Ile Arg Asp Pro Ser Lys Ala Leu Lys Glu Lys
            330                 335                 340

gtg tca aac gac gcc aag gat tta ttc gag aac aaa att ggg cag ggt     1112
Val Ser Asn Asp Ala Lys Asp Leu Phe Glu Asn Lys Ile Gly Gln Gly
        345                 350                 355

act gtg gac ttc atc aat aac gaa att cgt gac cct agt aag gca tta     1160
Thr Val Asp Phe Ile Asn Asn Glu Ile Arg Asp Pro Ser Lys Ala Leu
    360                 365                 370

ata aga aaa gtg tca acg ggg gcc gag gat tta ttc gag aac aaa att     1208
Ile Arg Lys Val Ser Thr Gly Ala Glu Asp Leu Phe Glu Asn Lys Ile
375                 380                 385                 390

ggg cag ggt act gtg gac ttc atc aat aac gaa att cgt gac cct agt     1256
Gly Gln Gly Thr Val Asp Phe Ile Asn Asn Glu Ile Arg Asp Pro Ser
                395                 400                 405

aag gca tta ata aga aaa gtg tac acc gag gcc gat gat tta ttc gag     1304
Lys Ala Leu Ile Arg Lys Val Tyr Thr Glu Ala Asp Asp Leu Phe Glu
            410                 415                 420

aac aaa att ggg cag ggt act gtg gac ttc atc aat aag gaa att cgt     1352
Asn Lys Ile Gly Gln Gly Thr Val Asp Phe Ile Asn Lys Glu Ile Arg
        425                 430                 435

gac cct agt aag gca tta ata aga aaa gtg tct acc gag gcc gat aat     1400
Asp Pro Ser Lys Ala Leu Ile Arg Lys Val Ser Thr Glu Ala Asp Asn
    440                 445                 450

tta ttg gag aaa taggttgcga agcccctgag gaagcaccgc aagggcaacg         1452
Leu Leu Glu Lys
455

ttagtgacag cggggaatct gaggaaattt cggctgtggg tgaatctttg gaatccgaca   1512

acgaaatgaa gacccaggag tcaatgaact cggagagtgc ttctaccgaa ctcccttctg   1572

aggagtccga ggaagagtcg gctgctatgg ttattcagca gcccaccctg gaggaggcca   1632

gccagatcgc attgcctgct gaagaagaca gctcagagtt gcaggaaacc tccgacaact   1692

atgaagcctc tctctagtca cctttgacgt ccatcgcact gctcggagaa tataaaacgc   1752

attgctcggt tgcactctag ttgttaacaa tgcacaattt aatgttatag ttgttttgaa   1812

aaaaaaaaaa aaaaaa                                                   1828
```

<210> 2
<211> 458
<212> PRT
<213> Babesia caballi

<400> 2

Met Ala Pro Ser Asp Ser Val Gly Asp Val Thr Lys Thr Leu Leu Ala
1 5 10 15

Ala Ser Glu Ser Val Asp Ser Ala Ala Asn Ala Tyr Met Ile Asn Ser
20 25 30

Asp Met Ser Asp Tyr Leu Ser Ala Val Ser Asp Asn Phe Ala Glu Arg
35 40 45

Ile Cys Ser Gln Val Pro Lys Gly Ser Asn Cys Ser Ala Ser Val Ser
50 55 60

Ala Tyr Met Ser Arg Cys Ala Lys Gln Asp Cys Leu Thr Leu Gln Ser
65 70 75 80

Leu Lys Tyr Pro Leu Glu Ala Lys Tyr Gln Pro Leu Thr Leu Pro Asp
85 90 95

Pro Tyr Gln Leu Glu Ala Ala Phe Ile Leu Phe Lys Glu Ser Asp Ala
100 105 110

Asn Pro Ala Asn Ser Thr Glu Lys Arg Phe Trp Met Arg Phe Arg Arg
115 120 125

Gly Lys Asn His Ser Tyr Phe His Asp Leu Val Phe Asn Leu Leu Glu
130 135 140

Lys Asn Val Thr Arg Asp Ala Asp Ala Thr Asp Ile Glu Asn Phe Ala
145 150 155 160

Ser Arg Tyr Leu Tyr Met Ala Thr Leu Tyr Tyr Lys Thr Tyr Thr Asn
165 170 175

Val Asp Glu Phe Gly Ala Ser Phe Phe Asn Lys Leu Ser Phe Thr Thr
180 185 190

Gly Leu Phe Gly Trp Gly Ile Lys Arg Ala Leu Lys Gln Ile Ile Arg
195 200 205

Ser Asn Leu Pro Leu Asp Ile Gly Thr Glu His Ser Val Ser Arg Leu
210 215 220

Gln His Ile Thr Ser Ser Tyr Lys Asp Tyr Met Asp Thr Gln Ile Pro
225   230   235   240

Ala Leu Pro Lys Phe Ala Lys Arg Phe Ser Leu Met Val Val Gln Arg
                245   250   255

Leu Leu Ala Thr Val Ala Gly Tyr Val Asp Thr Pro Trp Tyr Lys Lys
            260   265   270

Trp Tyr Met Lys Leu Lys Asn Phe Met Val Asn Arg Val Phe Ile Pro
        275   280   285

Thr Lys Lys Phe Phe Asn Lys Glu Ile Arg Glu Pro Ser Lys Ala Leu
    290   295   300

Lys Glu Lys Val Ser Thr Asp Thr Lys Asp Leu Phe Glu Asn Lys Ile
305   310   315   320

Gly Gln Gly Thr Val Asp Phe Phe Asn Lys Glu Ile Arg Asp Pro Ser
                325   330   335

Lys Ala Leu Lys Glu Lys Val Ser Asn Asp Ala Lys Asp Leu Phe Glu
            340   345   350

Asn Lys Ile Gly Gln Gly Thr Val Asp Phe Ile Asn Asn Glu Ile Arg
        355   360   365

Asp Pro Ser Lys Ala Leu Ile Arg Lys Val Ser Thr Gly Ala Glu Asp
    370   375   380

Leu Phe Glu Asn Lys Ile Gly Gln Gly Thr Val Asp Phe Ile Asn Asn
385   390   395   400

Glu Ile Arg Asp Pro Ser Lys Ala Leu Ile Arg Lys Val Tyr Thr Glu
                405   410   415

Ala Asp Asp Leu Phe Glu Asn Lys Ile Gly Gln Gly Thr Val Asp Phe
            420   425   430

Ile Asn Lys Glu Ile Arg Asp Pro Ser Lys Ala Leu Ile Arg Lys Val
        435   440   445

β1 Ser Thr Glu Ala Asp Asn Leu Leu Glu Lys
450 455
